

SEQUENCE LISTING

<110> Suntory Limited

<120> MARCHANTIALES-DERIVED UNSATURATED FATTY ACID SYNTHETASE GENES
AND USE OF THE SAME

<130>

<150> JP 2003-425673

<151> 2003-12-22

<160> 46

<170> PatentIn Ver. 2.1

<210> 1

<211> 2519

<212> DNA

<213> Marchantia polymorpha

<220>

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<222> (253)..(1698)

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Ser Arg Lys Glu Gln Gln Gln Gln Gln Ser Ser Pro Glu Ala

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Pro Glu Gly Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro
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agc gac tgc tgg atc gtc atc aac gac aag gtg tac gac gtg agc gca 531
Ser Asp Cys Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala
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Phe Gly Lys Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly
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Arg Asp Ala Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp
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Val Ser Glu Leu Val Lys Asp Tyr Arg Asp Leu Arg Thr Ala Phe Met
145 150 155

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Arg Ser Gln Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys
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Val Thr Glu Asn Arg Ser Leu Asn Thr Tyr Phe Gly Gly Leu Phe Trp
225 230 235

ggt aac ttc gcc cag ggc tac agc gtg gga tgg tgg aag acc aag cac 1011
Gly Asn Phe Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His
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aat gtg cac cac gcg gcc acg aac gaa tgc gac gac aag tat cag ccc 1059

Asn Val His His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro
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Ile Asp Pro Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu
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Gln His Leu Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp
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Leu His Ser Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr
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Met Arg Trp Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser
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Ile Gly Ala Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp
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Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu
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Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val
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Lys Ala Leu Cys Ala Lys His Gly Leu His Tyr Glu Glu Leu Ser Leu
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Ala Ala Lys Val
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<213> Marchantia polymorpha

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Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile Pro Glu Gly
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 Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro Ser Asp Cys
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 Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala Phe Gly Lys
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 Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly Arg Asp Ala
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 Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp Gln Phe Leu
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 Gln Asp Leu Tyr Ile Gly Asp Leu Tyr Asn Ala Glu Pro Val Ser Glu
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 Leu Val Lys Asp Tyr Arg Asp Leu Arg Thr Ala Phe Met Arg Ser Gln
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 Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys Val Thr Asn
 165 170 175
 Phe Ala Ile Leu Ala Ala Ser Leu Ala Val Ile Ala Trp Ser Gln Thr
 180 185 190
 Tyr Leu Ala Val Leu Cys Ser Ser Phe Leu Leu Ala Leu Phe Trp Gln
 195 200 205
 Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val Thr Glu
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 Asn Arg Ser Leu Asn Thr Tyr Phe Gly Gly Leu Phe Trp Gly Asn Phe
 225 230 235 240
 Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His Asn Val His
 245 250 255
 His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro Ile Asp Pro
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 Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu Ile Leu Ala
 275 280 285
 Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val Gln His Leu
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 Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp Leu His Ser
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 Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr Met Arg Trp
 325 330 335
 Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser Ile Gly Ala
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 Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp Leu Phe Leu
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 Ser Gln Leu Phe Cys Gly Ala Leu Leu Ser Ile Val Phe Val Ile Ser
 370 375 380
 His Asn Gly Met Asp Val Tyr Asn Asp Pro Arg Asp Phe Val Thr Ala
 385 390 395 400
 Gln Val Thr Ser Thr Arg Asn Ile Glu Gly Asn Phe Phe Asn Asp Trp
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 Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Ser
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 Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val Lys Ala Leu
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aggaggagca gcg atg gag gcg tac gag atg gtg gat agt ttt gtg tcg 229
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Thr Glu Ser Ala Ile Thr Lys Gly Leu Pro Cys Val Asp Ser Pro Thr
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ccg atc gtt ctt ggg ttg tgc tcc tac ttg aca ttc gtg ttt ctc ggg 373
Pro Ile Val Leu Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly
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ctc att gtc atc aag agc ctg gat ctt aag ccc cgc tcc aag gag ccc 421
Leu Ile Val Ile Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro
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Ala Ile Leu Asn Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala
80 85 90

ctc agt ctg tac atg tgc gtg gga att gtc cgt caa gct atc ctc aac 517
Leu Ser Leu Tyr Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn

95 100 105

agg tac tct ctg tgg ggc aat gcg tac aat ccc aaa gaa gtt caa atg 565
Arg Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met
110 115 120

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Gly His Leu Leu Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met
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145 150 155

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Leu His Val Tyr His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile
160 165 170

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Ala Tyr His Ala Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn
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Ser Gly Val His Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr
190 195 200

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Leu Gly Lys Asn Glu Lys Ala Arg Arg Lys Tyr Leu Trp Trp Gly Lys
205 210 215 220

tac ttg aca cag ctg cag atg ttc cag ttt gtc ctt aac atg att cag 901
Tyr Leu Thr Gln Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln
225 230 235

gct tac tac gat att aag aac aac tcg cct tac cca caa ttt ttg atc 949
Ala Tyr Tyr Asp Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile
240 245 250

cag att ttg ttc tac tac atg atc tcg ctt tta gcg cta ttt gga aac 997
Gln Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn
255 260 265

ttt tac gtt cac aaa tac gta tca gcg ccc gca aaa cct gcg aag atc 1045
Phe Tyr Val His Lys Tyr Val Ser Ala Pro Ala Lys Pro Ala Lys Ile
270 275 280

aag agc aaa aag gca gaa taa gacaccaccc tagtgacaag aagattttac 1096
Lys Ser Lys Lys Ala Glu
285 290

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 Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly Leu Ile Val Ile
 50 55 60
 Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro Ala Ile Leu Asn
 65 70 75 80
 Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala Leu Ser Leu Tyr
 85 90 95
 Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn Arg Tyr Ser Leu
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 Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met Gly His Leu Leu
 115 120 125
 Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met Asp Thr Val Ile
 130 135 140
 Met Ile Leu Lys Arg Asn Thr Arg Gln Ile Thr Val Leu His Val Tyr
 145 150 155 160
 His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile Ala Tyr His Ala
 165 170 175
 Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn Ser Gly Val His
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 Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr Leu Gly Lys Asn

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Ile	Lys	Asn	Asn	Ser	Pro	Tyr	Pro	Gln	Phe	Leu	Ile	Gln	Ile	Leu	Phe
245	250	255													
Tyr	Tyr	Met	Ile	Ser	Leu	Leu	Ala	Leu	Phe	Gly	Asn	Phe	Tyr	Val	His
260	265	270													
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Ala	Glu														
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 Pro Glu Val Phe Arg Leu Pro Asp Asp Ala Ile Pro Ala Gln Asp Arg
 15 20 25

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 Arg Ser Thr Gln Lys Lys Tyr Ser Leu Ser Asp Val Ser Lys His Asn
 30 35 40

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Thr Pro Asn Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val
45 50 55 60

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Thr Ser Trp Val Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys
65 70 75

gcg gga cag gat tca aca caa ctc ttt gat tct tat cac ccc ctc tat 650
Ala Gly Gln Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr
80 85 90

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Val Arg Lys Leu Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser
95 100 105

gcg gga gat gag aag ttc aag tct tca acg ttg gag tat gct ggt gaa 746
Ala Gly Asp Glu Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu
110 115 120

gaa cat gaa gta ttt tac cac act ctc aag cag cgc gtg gaa acg tac 794
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145 150 155

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Lys Ser Ala Val Ile Ile Gly Thr Leu Leu Cys Tyr Tyr Phe Gly
160 165 170

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175 180 185

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190 195 200

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205 210 215 220

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Ala Thr Leu Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln
225 230 235

cat gtg gcc ggg cac cac tcg ttc acc aac atc gac cat tac gat cca 1130
His Val Ala Gly His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro
(10)

240 245 250

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Tyr Gly Val Leu Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala
285 290 295 300

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305 310 315

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Leu Glu Met Gly Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr
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Ile Gly Leu Tyr Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala
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365 370 375 380

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Ala Glu Thr Asp Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu
385 390 395

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Thr His Ile Ser Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe
415 420 425

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Pro Gly Val Cys His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys
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Ala Thr Cys Asp Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe
445 450 455 460

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465 470 475

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Gln Asp Gly Leu Arg Leu Asp Gly
480 485

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accttcagg aacagaagtt gattcgaatg cgaaacctcc aatgagcatt tcacagccgt 2029
cttctccctg gccatcatgt gttccctcta gggagctcg gttttggaa gttagtcagc 2089
ttacttcga agatcgta acgctcaagg ctagatttg tcgacactat ttagttaggt 2149
ccgatagata ggtgataaga ttccggtgcc ctcacacatg tttcatcagt tgcgatgtaa 2209
ttccagtaat ccacgtatgt ggctccagtg tctgctgaaa tcagcacagg cagctatatac 2269
atgctccttg atctctaaaa aaaaaaaaaa aaaaaaaaa 2307

<210> 6
<211> 484
<212> PRT
<213> Marchantia polymorpha

<400> 6
Met Pro Pro His Ala Pro Asp Ser Thr Gly Leu Gly Pro Glu Val Phe
1 5 10 15
Arg Leu Pro Asp Asp Ala Ile Pro Ala Gln Asp Arg Arg Ser Thr Gln
20 25 30
Lys Lys Tyr Ser Leu Ser Asp Val Ser Lys His Asn Thr Pro Asn Asp
35 40 45
Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp Val
50 55 60
Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys Ala Gly Gln Asp
65 70 75 80
Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys Leu
85 90 95
Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser Ala Gly Asp Glu
100 105 110
Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu Glu His Glu Val

115	120	125	
Phe Tyr His Thr Leu Lys Gln Arg Val Glu Thr Tyr Phe Arg Lys Gln			
130	135	140	
Lys Ile Asn Pro Arg Tyr His Pro Gln Met Leu Val Lys Ser Ala Val			
145	150	155	160
Ile Ile Gly Thr Leu Leu Cys Tyr Tyr Phe Gly Phe Phe Trp Ser			
165	170	175	
Gln Asn Val Leu Leu Ser Met Phe Leu Ala Ser Ile Met Gly Phe Cys			
180	185	190	
Thr Ala Glu Val Gly Met Ser Ile Met His Asp Gly Asn His Gly Ser			
195	200	205	
Tyr Thr Gln Ser Thr Leu Leu Gly Tyr Val Met Gly Ala Thr Leu Asp			
210	215	220	
Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Ala Gly			
225	230	235	240
His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro Asp Ile Arg Val			
245	250	255	
Lys Asp Pro Asp Leu Arg Arg Val Thr Ser Gln Gln Pro Arg Arg Trp			
260	265	270	
Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu Tyr Gly Val Leu			
275	280	285	
Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala Phe Phe Ser Gly			
290	295	300	
Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro Leu Glu Met Gly			
305	310	315	320
Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr Met Phe Leu Leu			
325	330	335	
Pro Met Met Tyr Gly Gln Tyr Asn Ile Leu Thr Phe Ile Gly Leu Tyr			
340	345	350	
Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala Leu Phe Phe Gln			
355	360	365	
Val Ala His Val Val Asp Asp Ala Val Phe Pro Val Ala Glu Thr Asp			
370	375	380	
Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu Met Gln Val Arg			
385	390	395	400
Thr Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp Thr His Ile Ser			
405	410	415	
Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe Pro Gly Val Cys			
420	425	430	
His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys Ala Thr Cys Asp			
435	440	445	
Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe Trp Ala Ala Leu			
450	455	460	
Arg Ala His Phe Gln His Leu Lys Asn Val Gly Leu Gln Asp Gly Leu			
465	470	475	480
Arg Leu Asp Gly			

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
<221> n
<222> (12)

<400> 7
tggtggaarg anaarcayaa 20

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
<221> modified_base
<222> (4)
<223> i

<220>
<221> modified_base
<222> (7)
<223> i

<220>
<221> modified_base
<222> (10)
<223> i

<220>
<221> modified_base
<222> (13)
<223> i

<400> 8
rttnarnccn ccngtraacc a 21

<210> 9
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 9

aagttgcctt cgatgttct gg

22

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 10

gctcgccctgg agcaaggaaa tc

22

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> modified_base

<222> (3)

<223> i

<220>

<221> modified_base

<222> (18)

<223> i

<400> 11

gtngarttya tggayacngt

20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

(15)

<220>
<221> modified_base
<222> (3)
<223> i

<220>
<221> modified_base
<222> (12)
<223> i

<400> 12
cknccccara anarrraytt

20

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 13
gcgagctttc tcgttctttc cc

22

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 14
tatgattttg aagcgcaaca cg

22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
<221> modified_base
<222> (6)

(16)

<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
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<222> (14)
<223> i

<400> 15
athrangma arntaygay gt

22

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (3)
<223> i

<220>
<221> modified_base
<222> (6)
<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<400> 16
ggnaynkwnt sdatrcngg rtc

23

<210> 17
<211> 22

(17)

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 17
gtgtgtacga tccgtggtta cc 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 18
aaggcgggac aggattcaac ac 22

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 19
ggaattcgcg atggcctcgt ccaccaccac 30

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 20
ggaattctac tttcgacgatcgtatgcattac 29

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 21
ggaattcgcg atggaggcgt acgagatgg 29

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 22
ggaattcttc tgcccttttg ctcttgatc 29

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 23
gttgaattcg acagttatgc cgccacacgc 30

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 24
gttgaattca ggcccaaagc atgctgtcac 30

<210> 25
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer
<400> 25
cgggatcctc tcctggcgca ccatcgtc 28

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer
<400> 26
ggggtagccaa cgcgcttcc caccaacg 28

<210> 27
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer
<400> 27
gctctagagc gatggcctcg tccaccacc 29

<210> 28
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer
<400> 28
gctctagact atacttcgc agcgtatgc 29

<210> 29
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 29
gctctagagc gatggaggcg tacgagatgg 30

<210> 30
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 30
gctctagatt attctgcctt tttgctc 27

<210> 31
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 31
gctctagaga cagttatgcc gccacacgc 29

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 32
gctctagaag gcccaaagca tgctgtcac 29

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 33
cagggaaacag ctatgacc 18
(21)

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 34
aaactgcaga ttcccgatct agtaacatag 30

<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 35
ccggaattcg catgcctgca ggtcccccaga 30

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 36
tgtaaaacga cggccagt 18

<210> 37
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<221> Xaa
<222> (4)
<223> Description of Unknown Organism:conserved amino acid sequence

<400> 37

Trp Trp Lys Xaa Lys His Asn
1 5

<210> 38
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<400> 38
Trp Phe Thr Gly Gly Leu Asn
1 5

<210> 39
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<400> 39
Val Glu Phe Met Asp Thr Val
1 5

<210> 40
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<400> 40
Lys Tyr Leu Phe Trp Gly Arg
1 5

<210> 41
<211> 8
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<220>
<221> Xaa
<222> (2)
<223> Glu or Asn

<220>
<221> Xaa
<222> (3)
<223> Gly or Asp

<400> 41
Ile Xaa Xaa Lys Val Tyr Asp Val
1 5

<210> 42
<211> 8
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<220>
<221> Xaa
<222> (5)
<223> Gln or Asp

<220>
<221> Xaa
<222> (6)
<223> Tyr or Thr

<220>
<221> Xaa
<222> (7)
<223> Met or Val

<400> 42
Asp Pro Asp Ile Xaa Xaa Xaa Pro
1 5

<210> 43

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
XbaMpELOf

<400> 43
agtctctaga gcgatggagg cgtacg 26

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
SacMpELOr

<400> 44
cagtgagctc ggtgtcttat tctgcc 26

<210> 45
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer XbaMpD5f

<400> 45
agcttctaga gccatgccgc cacacgccc 29

<210> 46
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SacMpD5r

<400> 46
cagtgagctc tcagccatcc agtcgt 26